

aiImageStackAlignator

aiImageStackAlignator aligns either a single movie stack to a single image or a set of movie stacks to a tilt series. For latter, input is either a text file listing all needed parameters or a MDOC file.

For tilt series, aiImageStackAlignator also performs the initial data import to the Artiatomi package setting microscope dependent parameters. These values are either provided in a microscope specific configuration in ‘artiatomi.settings’ (ARTIATOMI_PATH env. variable must be set), in a microscope settings file or in case of a text file, which lists all input images with associated parameters.

aiImageStackAlignator can be used without a configuration file and all parameters can be provided by command line arguments. For convenience, parameters can also be given using a configuration file with the **-u** command line argument. Note: If a parameter is passed by file and by command line, the command line overrides the file.

Options are:

CudaDeviceID

The deviceID of the GPU to use.

Argument for command line: **-d** or **--CudaDeviceID**

Type: **int**

Option is mandatory: **false**

Default value if not set: **0**

Input

The file to process.

Argument for command line: **-i** or **--Input**

Type: **string**

Option is mandatory: **true**

Interpolation

Interpolation method to use.

Argument for command line: **-interp** or **--Interpolation**

Type: one of [**CUBIC**, **LINEAR**, **NN**]

Option is mandatory: **false**

Default value if not set: **NN**

Possible notations:

- **CUBIC**: CUBIC, cubic, Cubic
- **LINEAR**: LINEAR, linear, Linear
- **NN**: NN, nn, NearestNeighbor

LP

Low pass filter value.

Argument for command line: **-lp** or **--LP**

Type: **float**

Option is mandatory: **true**

LPS

Low pass filter sigma value.

Argument for command line: **-lps** or **--LPS**

Type: **float**
Option is mandatory: **true**

HP

High pass filter value.
Argument for command line: **-hp** or **--HP**
Type: **float**
Option is mandatory: **false**
Default value if not set: **0**

HPS

High pass filter sigma value.
Argument for command line: **-hps** or **--HPS**
Type: **float**
Option is mandatory: **false**
Default value if not set: **0**

MicroscopeID

Numeric identifier for the microscope used.
Argument for command line: **-scopeID** or **--MicroscopeID**
Type: **int**
Option is mandatory: **false**
Default value if not set: **-1**

MicroscopeName

Name identifier for the microscope used.
Argument for command line: **-scopeName** or **--MicroscopeName**
Type: **string**
Option is mandatory: **false**
Default value if not set: **"**

MicroscopeSettings

Use this additional settings file for this dataset.
Argument for command line: **-settings** or **--MicroscopeSettings**
Type: **string**
Option is mandatory: **false**
Default value if not set: **"**

DeadPixelRemoval

Enables removal of dead pixels based on thresholding. If set to 'relative', the threshold is X times the STD + MEAN of the image.
Argument for command line: **-deadPixel** or **--DeadPixelRemoval**
Type: one of [**ABSOLUTE**, **NONE**, **RELATIVE**]
Option is mandatory: **false**
Default value if not set: **NONE**
Possible notations:

- **ABSOLUTE**: ABSOLUTE, Absolute, absolute
- **NONE**: NONE, None, none

- **RELATIVE**: RELATIVE, Relative, relative

DeadPixelThreshold

Threshold above which a pixel is considered invalid.

Argument for command line: **-threshold** or **--DeadPixelThreshold**

Type: **float**

Option is mandatory: **true**

Only applicable if

- **DeadPixelRemoval** = ABSOLUTE or
- **DeadPixelRemoval** = RELATIVE

Output

The file to write the result to. If not provided the input file is appended by 'Alig'

Argument for command line: **-o** or **--Output**

Type: **string**

Option is mandatory: **false**

Default value if not set: **"**

MaxShift

Maximum allowed shift.

Argument for command line: **-m** or **--MaxShift**

Type: **int**

Option is mandatory: **false**

Default value if not set: **0**

AlignmentMethod

Either full alignment or blockwise alignment. When using global alignment, the number of correlations to compute can be reduced by only filling blocks of the CC-matrix.

Argument for command line: **-method** or **--AlignmentMethod**

Type: one of [**BLOCK**, **FULL**]

Option is mandatory: **false**

Default value if not set: **FULL**

Possible notations:

- **BLOCK**: BLOCK, block, Block
- **FULL**: FULL, full, Full

BlockSize

The block size to use for blocked alignment (only for global alignment).

Argument for command line: **-bs** or **--BlockSize**

Type: **int**

Option is mandatory: **true**

Only applicable if **AlignmentMethod** = BLOCK.

OutputDataType

The datatype of the aligned image.

Argument for command line: **-dt** or **--OutputDataType**

Type: one of [**FLOAT**, **SHORT**, **UCHAR**, **USHORT**]

Option is mandatory: **false**

Default value if not set: **USHORT**

Possible notations:

- **FLOAT**: FLOAT, float, Float
- **SHORT**: SHORT, short, Short
- **UCHAR**: UCHAR, uchar, Uchar, UChar
- **USHORT**: USHORT, ushort, Ushort, UShort

Algorithm

The algorithm to use: Global alignment (as in doi:10.1038/nmeth.2472), Refine (One-To-All approach), both, or skip alignment summing up with previously determined shifts.

Argument for command line: **-algo** or **--Algorithm**

Type: one of [**BOTH**, **GLOBAL**, **REFINE**, **SKIP**]

Option is mandatory: **false**

Default value if not set: **BOTH**

Possible notations:

- **BOTH**: BOTH, both, Both
- **GLOBAL**: GLOBAL, global, Global
- **REFINE**: REFINE, refine, Refine
- **SKIP**: SKIP, skip, Skip

CorrectMissingStripes

It can happen that K2 images have stripes with missing data. Enable this option if the dataset contains such stripes.

Argument for command line: **-stripes** or **--CorrectMissingStripes**

Type: **bool**

Option is mandatory: **false**

Default value if not set: **false**

SubpixelPrecision

Amount of sub-pixel precision: 2 is half pixel, 4 is a quarter pixel, etc. ≤ 1 to disable.

Argument for command line: **-subpix** or **--SubpixelPrecision**

Type: **int**

Option is mandatory: **false**

Default value if not set: **0**

OutputScaling

Factor to apply to the output image before potential conversion to integer.

Argument for command line: **-scaling** or **--OutputScaling**

Type: **float**

Option is mandatory: **false**

Default value if not set: **1**

OutputOffset

Offset to add to the output image before potential conversion to integer.

Argument for command line: **-offset** or **--OutputOffset**

Type: **float**

Option is mandatory: **false**

Default value if not set: **0**

RefineThreshold

Maximal shift allowed for refined alignment.

Argument for command line: **-rt** or **--RefineThreshold**

Type: **float**

Option is mandatory: **true**

Only applicable if

- **Algorithm** = BOTH or
- **Algorithm** = REFINE

DeadPixelMap

An image indicating defective pixels (same size as movie frames).

Argument for command line: **-deadPixelMap** or **--DeadPixelMap**

Type: **string**

Option is mandatory: **false**

Default value if not set: **"**

GainReference

An image for gain reference (same size as movie frames).

Argument for command line: **-gainRef** or **--GainReference**

Type: **string**

Option is mandatory: **false**

Default value if not set: **"**

Skip

Skip the X first frames of a stack (they still get aligned, but not stacked in the final step).

Argument for command line: **-skip** or **--Skip**

Type: **int**

Option is mandatory: **false**

Default value if not set: **0**

SkipShift

Skip frames with an incremental shift larger than the given limit (in pixels). The frames still get aligned, but not stacked in the final step.

Argument for command line: **-skipShift** or **--SkipShift**

Type: **float**

Option is mandatory: **false**

Default value if not set: **0**

DosePerTilt

The exposed dose of each tilt. Value to be written in the metadata file for tilt series.

Argument for command line: **-dose** or **--DosePerTilt**

Type: **float**

Option is mandatory: **false**

Default value if not set: **0**

AdditionalDoseFirstTilt

Additional dose for the first tilt due to extra measurements or longer exposure. Value to be written in the metadata file for tilt series.

Argument for command line: **-extradose** or **--AdditionalDoseFirstTilt**
Type: **float**
Option is mandatory: **false**
Default value if not set: **0**

FrameMetadata

Frame metadata for a tilt series can be stored inside the tilt series metadata file or in an additional file. Only used if output is a tilt series.

Argument for command line: **-meta** or **--FrameMetadata**
Type: **string**
Option is mandatory: **false**
Default value if not set: **"**

TomogramNumber

The number of this tilt series / tomogram in a dataset.

Argument for command line: **-tomo** or **--TomogramNumber**
Type: **int**
Option is mandatory: **false**
Default value if not set: **-1**